

SEQUENCE LISTING

<110> DUSCH, Nicole
THOMAS, Hermann
THIERBACH, Georg

<120> PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENOIC
ACID USING CORYNEFORM BACTERIA

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<150> DE 10048604.5

<151> 2000-09-30

<150> DE 10117085.8

<151> 2001-04-06

<160> 14

<170> PatentIn version 3.1

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<213> Corynebacterium glutamicum

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aagcgtggca acaactggaa tttaagagca caattgaagt cgcaccaagt taggcaacac
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aatagccata acgttgagga gttcag atg gca cac agc tac gca gaa caa tta
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Met Ala His Ser Tyr Ala Glu Gln Leu

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att gac act ttg gaa gct caa ggt gtg aag cga att tat ggt ttg gtg
401

Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val

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ggg gac agc ctt aat ccg atc gtg gat gct gtc cgc caa tca gat att
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Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile

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gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg ttt gca gcc ggt
497

Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala Phe Ala Ala Gly

45

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gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt gct gct tct tgt
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Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys

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ggg cct gga aac aca cac ctg att cag ggt ctt tat gat tcg cat cga
593

Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr Asp Ser His Arg

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aat ggt gcg aag gtg ttg gcc atc gct agc cat att ccg agt gcc cag
641

Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile Pro Ser Ala Gln

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95

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105

att ggt tgc acg ttc ttc cag gaa acg cat ccg gag att ttg ttt aag

689

Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu Ile Leu Phe Lys

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115

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gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt gag cag ggt gaa

737

Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly Glu Gln Gly Glu

125

130

135

cgc att ttg cat cac gcg att cag tcc acc atg gcg ggt aaa ggt gtg

785

Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala Gly Lys Gly Val

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tgc gtg gta gtg att cct ggt gat atc gct aag gaa gac gca ggt gac

833

Ser Val Val Val Ile Pro Gly Asp Ile Ala Lys Glu Asp Ala Gly Asp

155

160

165

ggt act tat tcc aat tcc act att tct tct ggc act cct gtg gtg ttc

881

Gly Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr Pro Val Val Phe

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180

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ccg gat cct act gag gct gca gcg ctg gtg gag gcg att aac aac gct

929

Pro Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala Ile Asn Asn Ala

190

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aag tct gtc act ttg ttc tgc ggt gcg ggc gtg aag aat gct cgc gcg

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Lys Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys Asn Ala Arg Ala

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215

cag gtg ttg gag ttg gcg gag aag att aaa tca ccg atc ggg cat gcg
1025

Gln Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro Ile Gly His Ala

220

225

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ctg ggt ggt aag cag tac atc cag cat gag aat ccg ttt gag gtc ggc
1073

Leu Gly Gly Lys Gln Tyr Ile Gln His Glu Asn Pro Phe Glu Val Gly

235

240

245

atg tct ggc ctg ctt ggt tac ggc gcc tgc gtg gat gcg tcc aat gag
1121

Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp Ala Ser Asn Glu

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255

260

265

gcg gat ctg ctg att cta ttg ggt acg gat ttc cct tat tct gat ttc
1169

Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro Tyr Ser Asp Phe

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275

280

ctt cct aaa gac aac gtt gcc cag gtg gat atc aac ggt gcg cac att
1217

Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn Gly Ala His Ile

285

290

295

ggc cga cgt acc acg gtg aag tat ccg gtg acc ggt gat gtt gct gca
1265

Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly Asp Val Ala Ala

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305

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aca atc gaa aat att ttg cct cat gtg aag gaa aaa aca gat cgt tcc
1313

Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys Thr Asp Arg Ser

315

320

325

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1361

Phe Leu Asp Arg Met Leu Lys Ala His Glu Arg Lys Leu Ser Ser Val

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335

340

345

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1409

Val Glu Thr Tyr Thr His Asn Val Glu Lys His Val Pro Ile His Pro

350

355

360

gaa tac gtt gcc tct att ttg aac gag ctg gcg gat aag gat gcg gtg

1457

Glu Tyr Val Ala Ser Ile Leu Asn Glu Leu Ala Asp Lys Asp Ala Val

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370

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ttt act gtg gat acc ggc atg tgc aat gtg tgg cat gcg agg tac atc

1505

Phe Thr Val Asp Thr Gly Met Cys Asn Val Trp His Ala Arg Tyr Ile

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gag aat ccg gag gga acg cgc gac ttt gtg ggt tca ttc cgc cac ggc

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Glu Asn Pro Glu Gly Thr Arg Asp Phe Val Gly Ser Phe Arg His Gly

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acg atg gct aat gcg ttg cct cat gcg att ggt gcg caa agt gtt gat

1601

Thr Met Ala Asn Ala Leu Pro His Ala Ile Gly Ala Gln Ser Val Asp

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415

420

425

cga aac cgc cag gtg atc gcg atg tgt ggc gat ggt ggt ttg ggc atg

1649

Arg Asn Arg Gln Val Ile Ala Met Cys Gly Asp Gly Gly Leu Gly Met

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435

440

ctg ctg ggt gag ctt ctg acc gtt aag ctg cac caa ctt ccg ctg aag

1697

Leu Leu Gly Glu Leu Leu Thr Val Lys Leu His Gln Leu Pro Leu Lys

445

450

455

gct gtg gtg ttt aac aac agt tct ttg ggc atg gtg aag ttg gag atg
1745

Ala Val Val Phe Asn Asn Ser Ser Leu Gly Met Val Lys Leu Glu Met

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465

470

ctc gtg gag gga cag cca gaa ttt ggt act gac cat gag gaa gtg aat
1793

Leu Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His Glu Glu Val Asn

475

480

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ttc gca gag att gcg gcg gct gcg ggt atc aaa tcg gta cgc atc acc
1841

Phe Ala Glu Ile Ala Ala Ala Ala Gly Ile Lys Ser Val Arg Ile Thr

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495

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505

gat cgc aag aaa gtt cgc gag cag cta gct gag gca ttg gca tat cct
1889

Asp Pro Lys Lys Val Arg Glu Gln Leu Ala Glu Ala Leu Ala Tyr Pro

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515

520

gga cct gta ctg atc gat atc gtc acg gat cct aat gcg ctg tcg atc
1937

Gly Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn Ala Leu Ser Ile

525

530

535

cca cca acc atc acg tgg gaa cag gtc atg gga ttc agc aag gcg gcc
1985

Pro Pro Thr Ile Thr Trp Glu Gln Val Met Gly Phe Ser Lys Ala Ala

540

545

550

acc cga acc gtc ttt ggt gga gga gta gga gcg atg atc gat ctg gcc
2033

Thr Arg Thr Val Phe Gly Gly Gly Val Gly Ala Met Ile Asp Leu Ala

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560

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cgt tgc aac ata agg aat att cct act cca tgatgattga tacacctgct
2083

Arg Ser Asn Ile Arg Asn Ile Pro Thr Pro

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2160

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35 40 45

Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
50 55 60

Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
65 70 75 80

Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
85 90 95

Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
100 105 110

Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
115 120 125

Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
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Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly
145 150 155 160

Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr
165 170 175

Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala
180 185 190

Ala Leu Val Glu Ala Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys
195 200 205

Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu
210 215 220

Lys Ile Lys Ser Pro Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile
225 230 235 240

Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr
245 250 255

Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu
260 265 270

Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
275 280 285

Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
290 295 300

Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
305 310 315 320

His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
325 330 335

Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
340 345 350

Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
355 360 365

Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
370 375 380

Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
385 390 395 400

Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
405 410 415

His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
420 425 430

Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
435 440 445

Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
450 455 460

Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
465 470 475 480

Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
485 490 495

Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
500 505 510

Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
515 520 525

Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
530 535 540

Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
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720

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<222> (802)..(2538)

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660

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720

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780

ccataacgtt gaggagttca g atg gca cac agc tac gca gaa caa tta att
831

Met Ala His Ser Tyr Ala Glu Gln Leu Ile

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5

10

gac act ttg gaa gct caa ggt gtg aag cga att tat ggt ttg gtg ggt
879

Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val Gly

15

20

25

gac agc ctt aat ccg atc gtg gat gct gtc cgc caa tca gat att gag
927

Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile Glu

30

35

40

tgg gtg cac gtt cga aat gag gaa gcg gcg gcg ttt gca gcc ggt gcg
975

Trp Val His Val Arg Asn Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala

45

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55

gaa tcg ttg atc act ggg gag ctg gca gta tgt gct gct tct tgt ggt
1023

Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys Gly

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65

70

cct gga aac aca cac ctg att cag ggt ctt tat gat tcg cat cga aat
1071

Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr Asp Ser His Arg Asn

75

80

85

90

ggc ggc aag gtc ttg gcc atc gct agc cat att ccg agt gcc cag att
1119

Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile Pro Ser Ala Gln Ile

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100

105

ggc tcg acg ttc ttc cag gaa acg cat ccg gag att ttg ttt aag gaa
1167

Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu Ile Leu Phe Lys Glu

110

115

120

tgc tct ggc tac tgc gag atg gtc aat ggc ggc gag cag ggc gaa cgc
1215

Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly Glu Gln Gly Glu Arg

125

130

135

att ttg cat cac ggc att cag tcc acc atg ggc ggc aaa ggc gtc tcg
1263

Ile Leu His His Ala Ile Gln Ser Thr Met Ala Gly Lys Gly Val Ser

140

145

150

gtg gta gtc att cct ggc gat atc gct aag gaa gac gca ggc gac ggc
1311

Val Val Val Ile Pro Gly Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly

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160

165

170

act tat tcc aat tcc act att tct tct ggc act cct gtc gtc ttc ccg
1359

Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr Pro Val Val Phe Pro

175

180

185

gat cct act gag gct gca ggc ctg gtc gag ggc att aac aac gct aag
1407

Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala Ile Asn Asn Ala Lys

190

195

200

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1455
 Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys Asn Ala Arg Ala Gln
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 gtg ttg gag ttg gcg gag aag att aaa tca ccg atc ggg cat gcg ctg
 1503
 Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro Ile Gly His Ala Leu
 220 225 230
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 Gly Gly Lys Gln Tyr Ile Gln His Glu Asn Pro Phe Glu Val Gly Met
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 Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn Gly Ala His Ile Gly
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 1743
 Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly Asp Val Ala Ala Thr
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 atc gaa aat att ttg cct cat gtg aag gaa aaa aca gat cgt tcc ttc
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 Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys Thr Asp Arg Ser Phe

ctg ggt gag ctt ctg acc gtt aag ctg cac caa ctt ccg ctg aag gct
2175

Leu Gly Glu Leu Leu Thr Val Lys Leu His Gln Leu Pro Leu Lys Ala

445

450

455

gtg gtg ttt aac aac agt tct ttg ggc atg gtg aag ttg gag atg ctc
2223

Val Val Phe Asn Asn Ser Ser Leu Gly Met Val Lys Leu Glu Met Leu

460

465

470

gtg gag gga cag cca gaa ttt ggt act gac cat gag gaa gtg aat ttc
2271

Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His Glu Glu Val Asn Phe

475

480

485

490

gca gag att gcg gcg gct gcg ggt atc aaa tcg gta cgc atc acc gat
2319

Ala Glu Ile Ala Ala Ala Ala Gly Ile Lys Ser Val Arg Ile Thr Asp

495

500

505

ccg aag aaa gtt cgc gag cag cta gct gag gca ttg gca tat cct gga
2367

Pro Lys Lys Val Arg Glu Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly

510

515

520

cct gta ctg atc gat atc gtc acg gat cct aat gcg ctg tcg atc cca
2415

Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn Ala Leu Ser Ile Pro

525

530

535

cca acc atc acg tgg gaa cag gtc atg gga ttc agc aag gcg gcc acc
2463

Pro Thr Ile Thr Trp Glu Gln Val Met Gly Phe Ser Lys Ala Ala Thr

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545

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cga acc gtc ttt ggt gga gga gta gga gcg atg atc gat ctg gcc cgt
2511

Arg Thr Val Phe Gly Gly Gly Val Gly Ala Met Ile Asp Leu Ala Arg

555

560

565

570

tcg aac ata agg aat att cct act cca tga tga tga tacacctgct
2558

Ser Asn Ile Arg Asn Ile Pro Thr Pro

575

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2618

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<212> PRT

<213> Corynebacterium glutamicum

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35 40 45

Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
50 55 60

Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
65 70 75 80

Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
85 90 95

Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
100 105 110

Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
115 120 125

Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
130 135 140

Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly
145 150 155 160

Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr
165 170 175

Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala
180 185 190

Ala Leu Val Glu Ala Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys

195

200

205

Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu
210 215 220

Lys Ile Lys Ser Pro Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile
225 230 235 240

Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr
245 250 255

Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu
260 265 270

Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
275 280 285

Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
290 295 300

Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
305 310 315 320

His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
325 330 335

Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
340 345 350

Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
355 360 365

Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
370 375 380

Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
385 390 395 400

Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro

405

410

415

His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
 420 425 430

Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
 435 440 445

Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
 450 455 460

Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
 465 470 475 480

Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
 485 490 495

Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
 500 505 510

Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
 515 520 525

Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
 530 535 540

Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
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Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile
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Pro Thr Pro

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120

cgggtaccca aaagaagggc cgccatgagc aggggatatg cgttgatgat ccacaacgct
180

tgggtttcgg tggctgcgag ctgttcacgc agcagaggga gtgcgggtgta gagaatcgag
240

ttgtctacac cgatcagaaa gagaccaccg ctgataacgg cgaggaaagc ccaacgttgg
300

gttttcgtag gcgcttgccg ctgtaagggt tctgaagtca tggatcgtaa ctgtaacgaa
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tggtcgggtac agttacaact cttttgttgg tgttttagac cacggcgctg tgtggcgatt
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<211> 613

<212> DNA

<213> *Corynebacterium glutamicum*

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120

tacggacatc tttattgcat atccgctgta tctaaccgat catgcagtgc aacgcctgaa
180

cgcgatcccc ggagaaattt ccattggcgt ggattcggtg gagatggcac aggcgacggc
240

gggttttcgg gaagatatca aggctctgat tgaagtggat tcgggacatc gtagaagtg
300

agtcacggcg actgcttcag aattgagtca gatccgcgag gcgctgggca gcaggatgat
360

aggagtgttt acttttctct ggcattctta tggcccgagg aatggtgagc aggcagcagc
420

tgatgagctt caggctctaa acaacagcgt ccagcgactt gctggcggcc tgacttctgg
480

cggttctctg ccgtctgcgc agtttacaga cgcaatcgat gagatgcgac caggcgtgta
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600

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<220>
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20

<210> 9
<211> 48
<212> DNA
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<220>
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<210> 11
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<220>
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<400> 11
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<210> 12
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120

agctgttcac gcagcagagg gagtgcgggtg tagagaatcg agttgtctac accgatcaga
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gcctgtaagg tttctgaagt catggatcgt aactgtaacg aatggtcggt acagttacaa
300

ctcttttgtt ggtgttttag accacggcgc tgtgtggcga tttaagacgt cggaatcgt
360

aggggactgt cagcgtgggt cgggttcttt gaggcgctta gaggcgattc tgtgaggtca
420

ctttttgttg ggtcggggtc taaatttggc cagttttcga ggcgaccaga caggcgtgcc
480

cacgatgttt aaataggcga tcggtgggca tctgtgtttg gtttcgacgg gctgaaacca
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1080

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1260

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